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RAW SEQUENCE LISTING
PATENT APPLICATION US/08/167,628

DATE: 02/16/94
TIME: 13:53:25

INPUT SET: S866.raw

1 SEQUENCE LISTING
2

3 (1) General Information:

4
5 (i) APPLICANT: Grotendorst, Gary R.
6 Bradham Jr., Douglas M.,

7
8 (ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

9
10 (iii) NUMBER OF SEQUENCES: 2

11 (iv) CORRESPONDENCE ADDRESS:

12 (A) ADDRESSEE: Spensley Horn Jubas & Lubitz
13 (B) STREET: 4225 Executive Square, Suite 1400
14 (C) CITY: La Jolla
15 (D) STATE: CA
16 (E) COUNTRY: US
17 (F) ZIP: 92037

18 (v) COMPUTER READABLE FORM:

19 (A) MEDIUM TYPE: Floppy disk
20 (B) COMPUTER: IBM PC compatible
21 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
22 (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

23 (vi) CURRENT APPLICATION DATA:

24 (A) APPLICATION NUMBER: US/08/167,628
25 (B) FILING DATE:
26 (C) CLASSIFICATION:

27 (vii) PRIOR APPLICATION DATA:

28 (A) APPLICATION NUMBER: US/07/752,427
29 (B) FILING DATE:

30 (viii) ATTORNEY/AGENT INFORMATION:

31 (A) NAME: Wetherell, Jr. Ph.D., John W.
32 (B) REGISTRATION NUMBER: 31,678
33 (C) REFERENCE/DOCKET NUMBER: PD-1294

34 (ix) TELECOMMUNICATION INFORMATION:

35 (A) TELEPHONE: 619-455-5100
36 (B) TELEFAX: 619-455-5110

37 (2) INFORMATION FOR SEQ ID NO:1:

38 (i) SEQUENCE CHARACTERISTICS:

39 (A) LENGTH: 2075 base pairs
40 (B) TYPE: nucleic acid
41 (C) STRANDEDNESS: single
42 (D) TOPOLOGY: linear

ENTERED

RAW SEQUENCE LISTING
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TIME: 13:53:36

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52 (ii) MOLECULE TYPE: cDNA
53
54
55
56 (vii) IMMEDIATE SOURCE:
57 (B) CLONE: DB60R32
58
59 (ix) FEATURE:
60 (A) NAME/KEY: CDS
61 (B) LOCATION: 130..1177
62
63
64 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
65
66 CCCGGCCGAC AGCCCCGAGA CGACAGCCCG GCGCGTCCCG GTCCCCACCT CCGACCACCG 60
67
68 CCAGCGCTCC AGGCCCCGCG CTCCCCGCTC GCCGCCACCG CGCCCTCCGC TCCGCCCGCA 120
69
70 GTGCCAACCC ATG ACC GCC GCC AGT ATG GGC CCC GTC CGC GTC GCC TTC 168
71 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe
72 1 5 10
73
74 GTG GTC CTC CTC GCC CTC TGC AGC CGG CCG GCC GTC GGC CAG AAC TGC 216
75 Val Val Leu Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys
76 15 20 25
77
78 AGC GGG CCG TGC CGG TGC CCG GAC GAG CCG GCG CCG CGC TGC CCG GCG 264
79 Ser Gly Pro Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala
80 30 35 40 45
81
82 GGC GTG AGC CTC GTG CTG GAC GGC TGC GGC TGC TGC CGC GTC TGC GCC 312
83 Gly Val Ser Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala
84 50 55 60
85
86 AAG CAG CTG GGC GAG CTG TGC ACC GAG CGC GAC CCC TGC GAC CCG CAC 360
87 Lys Gln Leu Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His
88 65 70 75
89
90 AAG GGC CTC TTC TGT GAC TTC GGC TCC CCG GCC AAC CGC AAG ATC GGC 408
91 Lys Gly Leu Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly
92 80 85 90
93
94 GTG TGC ACC GCC AAA GAT GGT GCT CCC TGC ATC TTC GGT GGT ACG GTG 456
95 Val Cys Thr Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val
96 95 100 105
97
98 TAC CGC AGC GGA GAG TCC TTC CAG AGC AGC TGC AAG TAC CAG TGC ACG 504
99 Tyr Arg Ser Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr
100 110 115 120 125
101
102 TGC CTG GAC GGG GCG GTG GGC TGC ATG CCC CTG TGC AGC ATG GAC GTT 552

**RAW SEQUENCE LISTING
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INPUT SET: S866.raw

103	Cys Leu Asp Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val			
104	130	135	140	
105				
106	CGT CTG CCC AGC CCT GAC TGC CCC TTC CCG AGG AGG GTC AAG CTG CCC	600		
107	Arg Leu Pro Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro			
108	145	150	155	
109				
110	GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648		
111	Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr			
112	160	165	170	
113				
114	G TG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696		
115	Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly			
116	175	180	185	
117				
118	CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744		
119	Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu			
120	190	195	200	205
121				
122	TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792		
123	Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val			
124	210	215	220	
125				
126	ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840		
127	Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys			
128	225	230	235	
129				
130	ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888		
131	Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly			
132	240	245	250	
133				
134	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936		
135	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu			
136	255	260	265	
137				
138	CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984		
139	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly			
140	270	275	280	285
141				
142	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032		
143	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu			
144	290	295	300	
145				
146	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080		
147	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met			
148	305	310	315	
149				
150	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128		
151	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn			
152	320	325	330	
153				

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154 GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T 1177
155 Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
156 335 340 345
157
158 GAAGCCAGAG AGTGAGAGAC ATTAACTCAT TAGACTGGAA CTTGAACTGA TTCACATCTC 1237
159
160 ATTTTCCGT AAAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTT TCTAACTGGG 1297
161
162 GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC 1357
163
164 CCAGACACTG GTTTGAAGAA TGTTAAGACT TGACAGTGGG ACTACATTAG TACACAGCAC 1417
165
166 CAGAAATGTAT ATTAAGGTGT GGCTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT 1477
167
168 CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAAT TGAGAAGGAA 1537
169
170 AATTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC 1597
171
172 CAGCCATCAA GAGACTGAGT CAAGTTGTC CTTAAGTCAG AACAGCAGAC TCAGCTCTGA 1657
173
174 CATTCTGATT CGAATGACAC TGTTCAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT 1717
175
176 TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTA AAATTTATAT TGTAAATATT 1777
177
178 GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTAA 1837
179
180 AGTTGTTGT GCCTTTTAT TTTGTTTT AATGCTTGA TATTCATG TTAGCCTCAA 1897
181
182 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957
183
184 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTGCAAA 2017
185
186 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075
187
188
189 (2) INFORMATION FOR SEQ ID NO:2:
190
191 (i) SEQUENCE CHARACTERISTICS:
192 (A) LENGTH: 349 amino acids
193 (B) TYPE: amino acid
194 (D) TOPOLOGY: linear
195
196 (ii) MOLECULE TYPE: protein
197
198 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
199
200 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu
201 1 5 10 15
202
203 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro
204 20 25 30

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205
206 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser
207 35 40 45
208
209 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu
210 50 55 60
211
212 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu
213 65 70 75 80
214
215 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr
216 85 90 95
217
218 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser
219 100 105 110
220
221 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp
222 115 120 125
223
224 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro
225 130 135 140
226
227 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys
228 145 150 155 160
229
230 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly
231 165 170 175
232
233 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro
234 180 185 190
235
236 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala
237 195 200 205
238
239 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp
240 210 215 220
241
242 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg
243 225 230 235 240
244
245 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Cys
246 245 250 255
247
248 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly
249 260 265 270
250
251 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr
252 275 280 285
253
254 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu Pro Val Glu
255 290 295 300

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**RAW SEQUENCE LISTING
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256
257 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile
258 305 310 315 320
259
260 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe
261 325 330 335
262
263 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala
264 340 345
265

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**SEQUENCE VERIFICATION REPORT
PATENT APPLICATION US/08/167,628**

DATE: 02/16/94
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Line

Error

Original Text

PAGE: 1

**SEQUENCE MISSING ITEM REPORT
PATENT APPLICATION US/08/167,628**

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<< THERE ARE NO ITEMS MISSING >>

PAGE: 1

SEQUENCE CORRECTION REPORT
PATENT APPLICATION **US/08/167,628**

DATE: 02/16/94
TIME: 13:54:39

INPUT SET: S866.raw

Line

Original Text

Corrected Text